

SID4

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RESULT      2
S57294
LOCUS       S57294          250 bp      DNA           MAM           28-JUN-1993
DEFINITION  {D-loop region} [cattle, Mitochondrial, 250 nt].
ACCESSION   S57294
VERSION     S57294.1  GI:298691
KEYWORDS     .
SOURCE      cow.
  ORGANISM  Mitochondrion Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 250)
  AUTHORS   Madsen,C.S., Ghivizzani,S.C. and Hauswirth,W.W.
  TITLE     Protein binding to a single termination-associated sequence in the
            mitochondrial DNA D-loop region
  JOURNAL   Mol. Cell. Biol. 13 (4), 2162-2171 (1993)
  MEDLINE   93204962
  REMARK    GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbsq 127635] from the original journal article.
            This sequence comes from Fig. 2.
COMMENT     Sequence is identical to previously published sequence with
            exception of an A-to-G transition at position 16079.
FEATURES             Location/Qualifiers
     source           1..250
                     /organism="Bos taurus"
                     /organelle="mitochondrion"
                     /db_xref="taxon:9913"
BASE COUNT        92 a        46 c        34 g        78 t
ORIGIN

      Query Match          100.0%;  Score 46;  DB 3;  Length 250;
      Best Local Similarity 100.0%;  Pred. No. 1.8e-08;
      Matches 46;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 attatatgccccatgcatataagcaagtacatgacctctatagcag 46
      ||||||||||||||||||||||||||||||||||||||||||||
Db      73 ATTATATGCCCCATGCATATAAGCAAGTACATGACCTCTATAGCAG 118

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-continued

Ser	Phe	Asp	Leu	Leu	Leu	Ser	Ser	Lys	Asn	Gly	Val	Ala	Ala	Phe	His
65					70					75					80
Ala	Phe	Leu	Lys	Thr	Glu	Phe	Ser	Glu	Glu	Asn	Leu	Glu	Phe	Trp	Leu
			85						90					95	
Ala	Cys	Glu	Glu	Phe	Lys	Lys	Ile	Arg	Ser	Ala	Thr	Lys	Leu	Ala	Ser
		100						105					110		
Arg	Ala	His	Gln	Ile	Phe	Glu	Glu	Phe	Ile	Cys	Ser	Glu	Ala	Pro	Lys
		115				120						125			
Glu	Val	Asn	Ile	Asp	His	Glu	Thr	Arg	Glu	Leu	Thr	Arg	Met	Asn	Leu
	130					135					140				
Gln	Thr	Ala	Thr	Ala	Thr	Cys	Phe	Asp	Ala	Ala	Gln	Gly	Lys	Thr	Arg
145					150					155					160
Thr	Leu	Met	Glu	Lys	Asp	Ser	Tyr	Pro	Arg	Phe	Leu	Lys	Ser	Pro	Ala
			165					170						175	
Tyr	Arg	Asp	Leu	Ala	Ala	Gln	Ala	Ser	Ala	Ala	Ser	Ala	Thr	Leu	Ser
		180					185							190	
Ser	Cys	Ser	Leu	Asp	Gln	Pro	Ser	His	Thr						
	195					200		202							

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1223 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 171..351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATTTAGACCA ACTCAGGAAA TAGGTGCACA CAAGCAAACC ATGTGGTTAA AGCCTTTGGA	60
ACTGCTTTGA GCAAAGCTGT AGCTGATTTC ACAAATCAT CTGCAAAACC AGATTCTTAA	120
CACCTCCCTG CTGTGTATCT CATTTCTGCT GATGTGTGGT GCTTCATAAG ATG GGG	176
ACG TTA AGC ATG CAG CAA CTA CAG TCA TTT GTT CTC AGA GGT CTG GAC	224
CAA AGA GAA ACA AGA AAA GCT GGA GTC ACA CTA CCA AAG GCC GAA GCT	272
GAG CAA CAG AGC TCT GGA GTC AGC TGC CTG GGT TCA GCA TGC AGC GCT	320
GCC GTG GAC GAT CTG TCT CTC TTG CAT ATA T GACTTACCAG TTTTACTTTC	371
AGTCTCTCCA TTTCTAATTA AATGAGATGC AGAAATGCTG GTGCCTTGCT ATGATGTTTG	431
CAGTTATTAT TTCTAGGAAA AAAAATATTA TTGTTACTCA GTATCTGGTC TAGCTACTTG	491
GACAACTGGA CTATCCCCCT CCTTCAAGG GAGGGCAAAG CATTCAGAA AAGAACTAAG	551
TGCTATTTCT CTGCTTCAGG AATGTCTCCC GTATGTAAAA GAATGTGGCT TCAGGGAGTA	611
GCATGTGTTG TAAAGGTGGA TGGGTCTAAC TTCATGGACA GCTCTGACAT CCACTAGCTA	671
TGCCACCTGA TGCAAAACCAC TTGGGCTGTC TGCAGTTTCG TTTATCTTTC TGAATTTGGT	731
AATAACAACC ACCTGGCAAG ATCACTGTTA TGAATACGGA GGATCAAAGT TGTGAAGTTA	791
TTTGTAAAG TGAATGTTT TGAATAATGG ATTTTAACAG TGTGAGCGAA AAGTAGATT	851
TTGACATTTA TCAAGAGTTC AGCTAATGAA AACAAGTATG GATAATAGTT ACATAGAACT	911
GTCTACTTTA CTCAGTACTT TAGCATATGC TATTATATTT AATCTTCTTA AAAAGTAGGA	971
AATTATACAA GCCATGTATT GATATTATTG TGSTGGTTGT CGTTCTCAAT TACACACTGA	1031